

SEQUENCE LISTING

							_				,	N.	
<110>	Bristol-	Myers So	quibb	Comp	any						•		
<120>	A NOVEL PREDOMIN									PROT	EIN	EXPRESSE)
<130>	D0066NP												
<140> <141>	U.S. Ser 2001-12-		10/02	29,34	17						٠		
<150> <151>	US 60/25 2000-12-												
<160>	45												
<170>	PatentIn	version	n 3.2									· ·	
<210> <211> <212> <213>	2689	oiens											
<220> <221> <222>		.949)											
<400> cggac	1 gcgtg ggcg	gcgcagc (ctggct	gaco	c tga	atcct	gga	ccaç	gtgco	ccc ç	gacco	gcggcg	60
cgccg	gtgcc gcag	g atg cto Met Le	g gcc ı Ala	cag Gln	ccg Pro 5	cag Gln	cgg Arg	ctg Leu	ctc Leu	ttc Phe 10	atc Ile	ctg Leu	110
gac g Asp G	gc gcg gac ly Ala Asp 15	gag cto	g ccg ı Pro	gcg Ala 20	ctg Leu	Gly	ggc Gly	ccc Pro	gag Glu 25	gcc Ala	gcg Ala	ccc Pro	158
tgc a Cys T	ca gac cco hr Asp Pro 0	ttc ga	g gcg u Ala 35	gcg Ala	agc Ser	ggc Gly	gcg Ala	cgg Arg 40	gtg Val	cta Leu	ggc Gly	GJÀ ààà	206
ctg c Leu L 45	tg agt aag eu Ser Lys	g gcg ct s Ala Le 50	g ctg u Leu	ccc Pro	acg Thr	gcc Ala	ctc Leu 55	ctg Leu	ctg Leu	gtg Val	acc Thr	acg Thr 60	254
cgc g Arg A	cc gcc gcc la Ala Ala	c các gg Pro Gl 65	g agg y Arg	ctg Leu	cag Gln	ggc Gly 70	cgc Arg	ctg Leu	tgt Cys	tcc Ser	ccg Pro 75	cag Gln	302
tgc g Cys A	cc gag gto la Glu Val 80	g cgc gg Arg Gl	c ttc y Phe	tcc Ser	gac Asp 85	aag Lys	gac Asp	aag Lys	aag Lys	aag Lys 90	tat Tyr	ttc Phe	350
tac a	ag ttc ttc	cgg ga	t gag	agg	agg	gcc	gag	cgc	gcc	tac	cgc	ttc	398

Tyr	Lys	Phe 95	Phe	Arg	Asp	Glu	Arg 100	Arg	Ala	Glu	Arg	Ala 105	Tyr	Arg	Phe		
	aag Lys 110															4	46
tgc Cys 125	tgg Trp	atc Ile	gtg Val	tgc Cys	acc Thr 130	gtg Val	ctg Leu	cgc Arg	cag Gln	cag Gln 135	ctg Leu	gag Glu	ctc Leu	ggt Gly	cgg Arg 140	4	94
	ctg Leu															5	42
	acc Thr															5	90
	ggc Gly															6	38
	cgc Arg 190			_		_		_	_	_						6	86
	ggc Gly															7	34
	gtg Val															7	82
_	gag Glu				-	_			_	_	-	-				8	30
	agg Arg															8	78
	ccg Pro 270															9	26
	agc Ser															9	74
gtt Val	tca Ser	gag Glu	cgt Arg	gtg Val 305	aag Lys	cag Gln	gag Glu	gcc Ala	ctg Leu 310	cgg Arg	tgg Trp	gtg Val	cag Gln	gga Gly 315	cag Gln	10	22
	cag Gln															10	70

	3	320					325					330			
ggg ctc Gly Leu	gag g Glu A 335	gac Asp	acc Thr	gaa Glu	gag Glu	cca Pro 340	gag Glu	gag Glu	gag Glu	gag Glu	gag Glu 345	gga Gly	gag Glu	gag Glu	1118
ccc aac Pro Asn 350	tac c Tyr E	cca Pro	ctg Leu	gag Glu	ttg Leu 355	ctg Leu	tac Tyr	tgc Cys	ctg Leu	tac Tyr 360	gag Glu	acg Thr	cag Gln	gag Glu	1166
gac gcg Asp Ala 365															1214
cag cga Gln Arg		Arg													1262
gtg agg Val Arg	Cys C	tgc Cys 400	cct Pro	gct Ala	gga Gly	cag Gln	gca Ala 405	ctg Leu	cgg Arg	ctg Leu	atc Ile	agc Ser 410	tgc Cys	aga Arg	1310
ttg gtt Leu Val	gct g Ala A 415	gcg Ala	cag Gln	gag Glu	aag Lys	aag Lys 420	aag Lys	aag Lys	agc Ser	ctg Leu	ggg Gly 425	aag Lys	cgg Arg	ctc Leu	1358
cag gcc Gln Ala 430	agc o Ser I	ctg Leu	ggt Gly	ggc Gly	ggc Gly 435	agt Ser	tct Ser	caa Gln	ggc Gly	acc Thr 440	aca Thr	aaa Lys	caa Gln	ctg Leu	1406
cca gcc Pro Ala 445	tcc (Ser I	ctt Leu	ctt Leu	cat His 450	cca Pro	ctc Leu	ttt Phe	cag Gln	gca Ala 455	atg Met	act Thr	gac Asp	cca Pro	ctg Leu 460	1454
tgc cat Cys His	ctg a	Ser	agc Ser 465	ctc Leu	acg Thr	ctg Leu	tcc Ser	cac His 470	tgc Cys	aaa Lys	ctc Leu	cct Pro	gac Asp 475	gcg Ala	1502
gtc tgc Val Cys	Arg A	gac Asp 480	ctt Leu	tct Ser	gag Glu	gcc Ala	ctg Leu 485	agg Arg	gca Ala	gcc Ala	ccc Pro	gca Ala 490	ctg Leu	acg Thr	1550
gag ctg Glu Leu	ggc (Gly 1 495	ctc Leu	ctc Leu	cac His	aac Asn	agg Arg 500	ctc Leu	agt Ser	gag Glu	gcg Ala	gga Gly 505	ctg Leu	cgt Arg	atg Met	1598
ctg agt Leu Ser 510	gag (ggc Gly	cta Leu	gcc Ala	tgg Trp 515	ccg Pro	cag Gln	tgc Cys	agg Arg	gtg Val 520	cag Gln	acg Thr	gtc Val	agg Arg	1646
gta cag Val Gln 525	ctg (Leu I	cct Pro	gac Asp	ccc Pro 530	cag Gln	cga Arg	ggg Gly	ctc Leu	cag Gln 535	tac Tyr	ctg Leu	gtg Val	ggt Gly	atg Met 540	1694
ctt cgg Leu Arg	cag a	agc Ser	ccc Pro 545	gcc Ala	ctg Leu	acc Thr	acc Thr	ctg Leu 550	gat Asp	ctc Leu	agc Ser	ggc Gly	tgc Cys 555	caa Gln	1742

														cac His		1790
														agc Ser		1838
_			_	-		_	-		_	_	_	_	_	gat Asp		1886
														aag Lys		1934
		_	acc Thr		tgaç	ggcto	ctg q	gtggd	ccaga	ag ca	agggt	ggaa	a ga	cccta	agtc	1989
aaag	gtcc	ctg 1	tgga	gagaa	ac g	gecea	attco	c aaq	gggca	agga	ggat	atto	gct (ctcg	gccttt	2049
ggga	aaact	ctt 1	tgago	ccga	ga go	gccgo	cagao	c ago	gcato	gtgg	gag	jccca	aga (cacgo	gcaccc	2109
tgc	cccgt	cc a	aggad	caggo	cc ca	aggad	cctgo	ccc	ctcto	ctcc	acad	cctg	ggg .	tacco	ccttct	2169
ccc	ccago	ccc o	cacca	actad	ct co	cacco	cacct	tco	ctcto	cctg	agad	cct	cca (gccat	tcccc	2229
ttga	aaaa	cac o	cccc	cgaco	cc ca	aagco	cacaa	a taa	atgad	cagc	gaga	agcto	cca (attaa	actaag	2289
caco	ctaco	ctg d	gcggd	cagaa	at aa	accct	tcad	c tgo	cctga	atcc	ccat	ctgo	cag	tgtgg	jcccaa	2349
cago	cccc	cag a	aacta	atgco	cc ad	cataç	gacto	g gaq	ggtag	ggca	gtto	cacco	gtc	cctc	ctgtt	2409
agga	aatga	aga d	ccato	ccct	ga go	gctat	ggc	caq	ggcco	caca	ggc	gtcca	agt (gtctç	gagatc	2469
tttç	gggaa	agg (gagad	ctage	gg ca	aggto	ggaga	a caç	gcgca	agaa	ccc	ccgt	gct (gggt	ggaag	2529
cato	gacca	aca t	tggt	gggt	ga go	cagco	ccca	a tgo	cacto	gacg	gtaa	atto	ccc (ctgt	ggactc	2589
attt	ctgt	tg q	gttt	ctatt	ta ca	acct	gcca	a ggo	cgtg	gtac	aata	acago	gtc (ggtgd	ctcaca	2649
aaaa	aaaa	aaa a	aaaa	aaaa	aa aa	aaaa	aaaa	a aaa	aaaa	aaaa						2689

<210> 2 <211> 625 <212> PRT <213> homo sapiens

<400> 2

Met Leu Ala Gln Pro Gln Arg Leu Leu Phe Ile Leu Asp Gly Ala Asp 5 15 10

- Glu Leu Pro Ala Leu Gly Gly Pro Glu Ala Ala Pro Cys Thr Asp Pro 20 25 30
- Phe Glu Ala Ala Ser Gly Ala Arg Val Leu Gly Gly Leu Leu Ser Lys 35 40 45
- Ala Leu Leu Pro Thr Ala Leu Leu Val Thr Thr Arg Ala Ala 50 55 60
- Pro Gly Arg Leu Gln Gly Arg Leu Cys Ser Pro Gln Cys Ala Glu Val 65 70 75 80
- Arg Gly Phe Ser Asp Lys Asp Lys Lys Lys Tyr Phe Tyr Lys Phe Phe 85 90 95
- Arg Asp Glu Arg Arg Ala Glu Arg Ala Tyr Arg Phe Val Lys Glu Asn 100 105 110
- Glu Thr Leu Phe Ala Leu Cys Phe Val Pro Phe Val Cys Trp Ile Val 115 120 125
- Cys Thr Val Leu Arg Gln Gln Leu Glu Leu Gly Arg Asp Leu Ser Arg 130 135 140
- Thr Ser Lys Thr Thr Thr Ser Val Tyr Leu Leu Phe Ile Thr Ser Val 145 150 155 160
- Leu Ser Ser Ala Pro Val Ala Asp Gly Pro Arg Leu Gln Gly Asp Leu 165 170 175
- Arg Asn Leu Cys Arg Leu Ala Arg Glu Gly Val Leu Gly Arg Ala 180 185 190
- Gln Phe Ala Glu Lys Glu Leu Glu Gln Leu Glu Leu Arg Gly Ser Lys 195 200 205
- Val Gln Thr Leu Phe Leu Ser Lys Lys Glu Leu Pro Gly Val Leu Glu 210 215 220
- Thr Glu Val Thr Tyr Gln Phe Ile Asp Gln Ser Phe Gln Glu Phe Leu 225 230 235 240
- Ala Ala Leu Ser Tyr Leu Leu Glu Asp Gly Gly Val Pro Arg Thr Ala

245 250 255

Ala Gly Gly Val Gly Thr Leu Leu Arg Gly Asp Ala Gln Pro His Ser 260 265 270

His Leu Val Leu Thr Thr Arg Phe Leu Phe Gly Leu Leu Ser Ala Glu 275 280 285

Arg Met Arg Asp Ile Glu Arg His Phe Gly Cys Met Val Ser Glu Arg 290 295 300

Val Lys Gln Glu Ala Leu Arg Trp Val Gln Gly Gln Gly Gln Gly Cys 305 310 315 320

Pro Gly Val Ala Pro Glu Val Thr Glu Gly Ala Lys Gly Leu Glu Asp 325 330 335

Thr Glu Glu Pro Glu Glu Glu Glu Glu Glu Glu Glu Pro Asn Tyr Pro 340 345 350

Leu Glu Leu Leu Tyr Cys Leu Tyr Glu Thr Gln Glu Asp Ala Phe Val 355 360 365

Arg Gln Ala Leu Cys Arg Phe Pro Glu Leu Ala Leu Gln Arg Val Arg 370 \$375\$ 380

Phe Cys Arg Met Asp Val Ala Val Leu Ser Tyr Cys Val Arg Cys Cys 385 390 395 400

Pro Ala Gly Gln Ala Leu Arg Leu Ile Ser Cys Arg Leu Val Ala Ala 405 410 415

Gln Glu Lys Lys Lys Ser Leu Gly Lys Arg Leu Gln Ala Ser Leu 420 425 430

Gly Gly Ser Ser Gln Gly Thr Thr Lys Gln Leu Pro Ala Ser Leu 435 440 445

Leu His Pro Leu Phe Gln Ala Met Thr Asp Pro Leu Cys His Leu Ser 450 460

Ser Leu Thr Leu Ser His Cys Lys Leu Pro Asp Ala Val Cys Arg Asp 465 470 475 480

Leu Ser Glu Ala Leu Arg Ala Ala Pro Ala Leu Thr Glu Leu Gly Leu 485 490 495

Leu His Asn Arg Leu Ser Glu Ala Gly Leu Arg Met Leu Ser Glu Gly 500 505 510

Leu Ala Trp Pro Gln Cys Arg Val Gln Thr Val Arg Val Gln Leu Pro 515 520 525

Asp Pro Gln Arg Gly Leu Gln Tyr Leu Val Gly Met Leu Arg Gln Ser 530 540

Pro Ala Leu Thr Thr Leu Asp Leu Ser Gly Cys Gln Leu Pro Ala Pro 545 550 555 560

Met Val Thr Tyr Leu Cys Ala Val Leu Gln His Gln Gly Cys Gly Leu 565 570 575

Gln Thr Leu Ser Leu Ala Ser Val Glu Leu Ser Glu Gln Ser Leu Gln 580 585 590

Glu Leu Gln Ala Val Lys Arg Ala Lys Pro Asp Leu Val Ile Thr His 595 600 605

Pro Ala Leu Asp Gly His Pro Gln Pro Pro Lys Glu Leu Ile Ser Thr 610 620

Phe 625

<210> 3

<211> 1429

<212> PRT

<213> homo sapiens

<400> 3

Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu 1 5 10 15

Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala 20 25 30

His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr 35 40 45

Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln 50 55 60

Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg 65 70 75 80

Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe 85 90 95

Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr 100 . 105 110

Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys 115 120 125

Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser 130 135 140

Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser His Leu Tyr Gln Ala Leu 145 150 155 160

Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala 165 170 175

Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro 180 185 190

Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu 195 200 205

Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg 210 215 220

Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr 225 230 235 240

Pro Pro Gln Ala His Ser Ser Leu Gln Pro His His Pro Trp Glu 245 250 255

Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu

260 265 270

- Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Gln Arg Pro His 275 280 285
- Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val 290 295 300
- Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro 305 310 315
- Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala 325 330 335
- Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly 340 345 350
- Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser 355 360 365
- Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile 370 375 380
- Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser 385 390 395 400
- Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly 405 410 415
- Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln 420 425 430
- Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile 435 440 445
- Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln 450 460
- Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly 465 470 475 480
- Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp 485 490 495

505 500 Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr 520 Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser 535 Lys Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln 555 550 Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala 570 Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly 600 Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu 615 Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu 630 Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr 650 Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg 660 665 Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn 680 Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val 695 700 Pro Ser Leu Gln Leu Leu Gln Pro His Ser Leu Glu Ser Leu His 705 710 715

Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu

Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Ser Met Val Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Met Asp Ala 880 . Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu

- Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln 945 955 960
- Thr Thr Leu Ser Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln 965 970 975
- Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met 980 985 990
- Thr Pro Ile Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser 995 1000 1005
- Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His 1010 1015 1020
- Val Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe 1025 1030 1035
- Pro Ile Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro 1040 1045 1050
- Val Glu Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu 1055 1060 1065
- His Thr Lys Pro Leu Gly Thr Asp Asp Asp Phe Trp Gly Pro Thr 1070 1075 1080
- Gly Pro Val Ala Thr Glu Val Val Asp Lys Glu Lys Asn Leu Tyr 1085 1090 1095
- Arg Val His Phe Pro Val Ala Gly Ser Tyr Arg Trp Pro Asn Thr 1100 1105 1110
- Gly Leu Cys Phe Val Val Arg Glu Ala Val Thr Val Glu Ile Glu 1115 1120 1125
- Phe Cys Val Trp Asp Gln Phe Leu Gly Glu Ile Asn Pro Gln His 1130 1135 1140
- Ser Trp Met Val Ala Gly Pro Leu Leu Asp Ile Lys Ala Glu Pro 1145 1150 1155
- Gly Ala Val Glu Ala Val His Leu Pro His Phe Val Ala Leu Gln

- 1160 1165 1170
- Gly Gly His Val Asp Thr Ser Leu Phe Gln Val Ala His Phe Lys 1175 1180 1185
- Glu Glu Gly Met Leu Leu Glu Lys Pro Ala Arg Val Glu Leu His 1190 1195 1200
- His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro Leu Gly Val Leu 1205 1210 1215
- Leu Lys Met Ile His Asn Ala Leu Arg Phe Ile Pro Val Thr Ser 1220 1225 1230
- Val Val Leu Leu Tyr His Arg Leu His Pro Glu Glu Val Thr Phe 1235 1240 1245
- His Leu Tyr Leu Ile Pro Ser Asp Cys Ser Ile Arg Lys Glu Leu 1250 1255 1260
- Glu Leu Cys Tyr Arg Ser Pro Gly Glu Asp Gln Leu Phe Ser Glu 1265 1270 1275
- Phe Tyr Val Gly His Leu Gly Ser Gly Ile Arg Leu Gln Val Lys 1280 1285 1290
- Asp Lys Lys Asp Glu Thr Leu Val Trp Glu Ala Leu Val Lys Pro 1295 1300 1305
- Gly Asp Leu Met Pro Ala Thr Thr Leu Ile Pro Pro Ala Cys Ile 1310 1315 1320
- Ala Val Pro Ser Pro Leu Asp Ala Pro Gln Leu Leu His Phe Val 1325 1330 1335
- Val Val Leu Asp Lys Leu His Gly Gln Val Leu Ser Gln Glu Gln 1355 1360 1365
- Tyr Glu Arg Val Leu Ala Glu Asn Thr Arg Pro Ser Gln Met Arg 1370 1375 1380

Lys Leu Phe Ser Leu Ser Gln Ser Trp Asp Arg Lys Cys Lys Asp 1385 1390 1395

Gly Leu Tyr Gln Ala Leu Lys Glu Thr His Pro His Leu Ile Met 1400 1405 1410

Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu Leu Pro Leu Ser 1415 1420 1425

Ser

<210> 4

<211> 1033

<212> PRT

<213> Homo sapiens

<400> 4

Met Gly Phe Asn Leu Gln Ala Leu Leu Glu Gln Leu Ser Gln Asp Glu $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Leu Ser Lys Phe Lys Tyr Leu Ile Thr Thr Phe Ser Pro Ala His Glu 20 25 30

Leu Gln Lys Ile Pro His Lys Glu Val Asp Lys Ala Asp Gly Lys Gln 35 40 45

Leu Val Glu Ile Leu Thr Thr His Cys Asp Ser Tyr Trp Val Glu Met 50 55 60

Ala Ser Leu Gln Val Phe Glu Lys Met His Arg Met Asp Leu Ser Glu 65 70 75 80

Arg Ala Lys Asp Glu Val Arg Glu Ala Ala Leu Lys Ser Phe Asn Lys 85 90 95

Arg Lys Pro Leu Ser Leu Gly Ile Thr Arg Lys Glu Arg Pro Pro Leu 100 105 110

Asp Val Asp Glu Met Leu Glu Arg Phe Lys Thr Glu Ala Gln Asp Lys 115 120 125

Asp Asn Arg Cys Arg Tyr Ile Leu Lys Thr Lys Phe Arg Glu Met Trp 135 140 Lys Ser Trp Pro Gly Asp Ser Lys Glu Val Gln Val Met Ala Glu Arg 150 155 Tyr Lys Met Leu Ile Pro Phe Ser Asn Pro Arg Val Leu Pro Gly Pro 170 165 Phe Ser Tyr Thr Val Val Leu Tyr Gly Pro Ala Gly Leu Gly Lys Thr Thr Leu Ala Gln Lys Leu Met Leu Asp Trp Ala Glu Asp Asn Leu Ile 200 His Lys Phe Lys Tyr Ala Phe Tyr Leu Ser Cys Arg Glu Leu Ser Arg 215 Leu Gly Pro Cys Ser Phe Ala Glu Leu Val Phe Arg Asp Trp Pro Glu 230 Leu Gln Asp Asp Ile Pro His Ile Leu Ala Gln Ala Arg Lys Ile Leu 250 Phe Val Ile Asp Gly Phe Asp Glu Leu Gly Ala Ala Pro Gly Ala Leu 260 265 Ile Glu Asp Ile Cys Gly Asp Trp Glu Lys Lys Lys Pro Val Pro Val , 280 Leu Leu Gly Ser Leu Leu Asn Arg Val Met Leu Pro Lys Ala Ala Leu Leu Val Thr Thr Arg Pro Arg Ala Leu Arg Asp Leu Arg Ile Leu Ala 310 315 Glu Glu Pro Ile Tyr Ile Arg Val Glu Gly Phe Leu Glu Glu Asp Lys 330 325 Arg Ala Tyr Phe Leu Arg His Phe Gly Asp Glu Asp Gln Ala Met Arg 345 Ala Phe Glu Leu Met Arg Ser Asn Ala Ala Leu Phe Gln Leu Gly Ser 355 360 365

- Ala Pro Ala Val Cys Trp Ile Val Cys Thr Thr Leu Lys Leu Gln Met 370 375 380
- Glu Lys Gly Glu Asp Pro Val Pro Thr Cys Leu Thr Arg Thr Gly Leu 385 390 395 400
- Phe Leu Arg Phe Leu Cys Ser Arg Phe Pro Gln Gly Ala Gln Leu Arg 405 410 415
- Gly Ala Leu Arg Thr Leu Ser Leu Leu Ala Ala Gln Gly Leu Trp Ala 420 425 430
- Gln Thr Ser Val Leu His Arg Glu Asp Leu Glu Arg Leu Gly Val Gln 435 440 445
- Glu Ser Asp Leu Arg Leu Phe Leu Asp Gly Asp Ile Leu Arg Gln Asp 450 455 460
- Arg Val Ser Lys Gly Cys Tyr Ser Phe Ile His Leu Ser Phe Gln Gln 465 470 475 480
- Phe Leu Thr Ala Leu Phe Tyr Thr Leu Glu Lys Glu Glu Glu Asp 485 490 495
- Arg Asp Gly His Thr Trp Asp Ile Gly Asp Val Gln Lys Leu Leu Ser 500 505
- Gly Val Glu Arg Leu Arg Asn Pro Asp Leu Ile Gln Ala Gly Tyr Tyr 515 520 525
- Ser Phe Gly Leu Ala Asn Glu Lys Arg Ala Lys Glu Leu Glu Ala Thr 530 535 540
- Phe Gly Cys Arg Met Ser Pro Asp Ile Lys Gln Glu Leu Leu Arg Cys 545 550 555 560
- Asp Ile Ser Cys Lys Gly Gly His Ser Thr Val Thr Asp Leu Gln Glu 565 570 575
- Leu Leu Gly Cys Leu Tyr Glu Ser Gln Glu Glu Glu Leu Val Lys Glu 580 585 590

Val Val Pro Ser Ser Phe Cys Val Lys His Cys Arg Asn Leu Gln Lys Met Ser Leu Gln Val Ile Lys Glu Asn Leu Pro Glu Asn Val Thr Ala Ser Glu Ser Asp Ala Glu Val Glu Arg Ser Gln Asp Asp Gln His Met Leu Pro Phe Trp Thr Asp Leu Cys Ser Ile Phe Gly Ser Asn Lys Asp Leu Met Gly Leu Ala Ile Asn Asp Ser Phe Leu Ser Ala Ser Leu Val Arg Ile Leu Cys Glu Gln Ile Ala Ser Asp Thr Cys His Leu Gln Arg Val Val Phe Lys Asn Ile Ser Pro Ala Asp Ala His Arg Asn Leu Cys Leu Ala Leu Arg Gly His Lys Thr Val Thr Tyr Leu Thr Leu Gln Gly Asn Asp Gln Asp Asp Met Phe Pro Ala Leu Cys Glu Val Leu Arg His Pro Glu Cys Asn Leu Arg Tyr Leu Gly Leu Val Ser Cys Ser Ala Thr Thr Gln Gln Trp Ala Asp Leu Ser Leu Ala Leu Glu Val Asn Gln Ser Leu Thr Cys Val Asn Leu Ser Asp Asn Glu Leu Leu Asp Glu Gly Ala

Lys Leu Leu Tyr Thr Thr Leu Arg His Pro Lys Cys Phe Leu Gln Arg

Val Met Ala Gln Phe Lys Glu Ile Ser Leu His Leu Asn Ala Val Asp

- Leu Ser Leu Glu Asn Cys His Leu Thr Glu Ala Asn Cys Lys Asp Leu 820 825 830
- Ala Ala Val Leu Val Val Ser Arg Glu Leu Thr His Leu Cys Leu Ala 835 840 845
- Lys Asn Pro Ile Gly Asn Thr Gly Val Lys Phe Leu Cys Glu Gly Leu 850 855 860
- Arg Tyr Pro Glu Cys Lys Leu Gln Thr Leu Val Leu Trp Asn Cys Asp 865 870 875 880
- Ile Thr Ser Asp Gly Cys Cys Asp Leu Thr Lys Leu Gln Glu Lys 885 890 895
- Ser Ser Leu Leu Cys Leu Asp Leu Gly Leu Asn His Ile Gly Val Lys 900 905 910
- Gly Met Lys Phe Leu Cys Glu Ala Leu Arg Lys Pro Leu Cys Asn Leu 915 920 925
- Arg Cys Leu Trp Leu Trp Gly Cys Ser Ile Pro Pro Phe Ser Cys Glu 930 935 940
- Asp Leu Cys Ser Ala Leu Ser Asn Gln Ser Leu Val Thr Leu Asp Leu 945 950 955 960
- Gly Gln Asn Pro Leu Gly Ser Ser Gly Val Lys Met Leu Phe Glu Thr 965 970 975
- Leu Thr Cys Ser Ser Gly Thr Leu Arg Thr Leu Arg Leu Lys Ile Asp 980 985 990
- Asp Phe Asn Asp Glu Leu Asn Lys Leu Leu Glu Glu Ile Glu Glu Lys 995 1000 1005
- Asn Pro Gln Leu Ile Ile Asp Thr Glu Lys His His Pro Trp Ala 1010 1015 1020
- Glu Arg Pro Ser Ser His Asp Phe Met Ile 1025 1030

<210> 5 <211> 2763 <212> DNA <213> Homo Sapiens

<400> cggacgcgtg ggcgcagc ctggctgacc tgatcctgga ccagtgcccc gaccgcggcg 60 cgccggtgcc gcagatgctg gcccagccgc agcggctgct cttcatcctg gacggcgcgg 120 180 acgagetgee ggegetgggg ggeeeegagg eegegeeetg cacagaceee ttegaggegg 240 cgagcggcgc gcgggtgcta ggcgggctgc tgagtaaggc gctgctgccc acggccctcc 300 tgctggtgac cacgcgcgcc gccgccccg ggaggctgca gggccgcctg tgttccccgc 360 agtgcgccga ggtgcgcggc ttctccgaca aggacaagaa gaagtatttc tacaagttct tccgggatga gaggaggcc gagcgccct accgcttcgt gaaggagaac gagacgctgt 420 480 tegegetgtg ettegtgeee ttegtgtget ggategtgtg eacegtgetg egecageage 540 tggagetegg tegggaeetg tegegeaegt ceaagaeeae eaegteagtg tacetgettt tcatcaccag cgttctgagc tcggctccgg tagccgacgg gccccggttg cagggcgacc 600 660 tgcgcaatct gtgccgcctg gcccgcgagg gcgtcctcgg acgcagggcg cagtttgccg agaaggaact ggagcaactg gagcttcgtg gctccaaagt gcagacgctg tttctcagca 720 780 aaaaggagct gccgggcgtg ctggagacag aggtcaccta ccagttcatc gaccagagct 840 tccaggagtt cctcgcggca ctgtcctacc tgctggagga cggcggggtg cccaggaccg 900 cggctggcgg cgttgggaca ctcctgcgtg gggacgccca gccgcacagc cacttggtgc tcaccacgcg cttcctcttc ggactgctga gcgcggagcg gatgcgcgac atcgagcgcc 960 1020 acttcggctg catggtttca gagcgtgtga agcaggaggc cctgcggtgg gtgcagggac 1080 agggacaggg ctgccccgga gtggcaccag aggtgaccga gggggccaaa gggctcgagg 1140 acaccgaaga gccagaggag gaggaggagg gagaggagcc caactaccca ctggagttgc tgtactgcct gtacgagacg caggaggacg cgtttgtgcg ccaagccctg tgccggttcc 1200 cggagctggc gctgcagcga gtgcgcttct gccgcatgga cgtggctgtt ctgagctact 1260 1320 gcgtgaggtg ctgccctgct ggacaggcac tgcggctgat cagctgcaga ttggttgctg cqcaqqaqaa qaaqaagaaq agcctgggga aqcqgctcca ggccagcctg ggtggcggca 1380 1440 gttctcaagg caccacaaaa caactgccag cctcccttct tcatccactc tttcaggcaa 1500 tgactgaccc actgtgccat ctgagcagcc tcacgctgtc ccactgcaaa ctccctgacg 1560 eggtetgeeg agacetttet gaggeeetga gggeageeee egeactgaeg gagetgggee

tcctccacaa	caggctcagt	gaggcgggac	tgcgtatgct	gagtgagggc	ctagcctggc	1620
cgcagtgcag	ggtgcagacg	gtcaggtgag	gcctggcctg	ggagggaccg	tgggatgccc	1680
ccgccacccc	agcagctcct	gaggtcggcc	ctcccacagg	gtacagctgc	ctgaccccca	1740
gcgagggctc	cagtacctgg	tgggtatgct	tcggcagagc	cccgccctga	ccaccctgga	1800
tctcagcggc	tgccaactgc	ccgcccccat	ggtgacctac	ctgtgtgcag	tcctgcagca	1860
ccagggatgc	ggcctgcaga	ccctcagtct	ggcctctgtg	gagctgagcg	agcagtcact	1920
acaggagctt	caggctgtga	agagagcaaa	gccggatctg	gtcatcacac	acccagcgct	1980
ggacggccac	ccacaacctc	ccaaggaact	catctcgacc	ttctgaggct	ctggtggcca	2040
gagcagggtg	gaagacccta	gtcaaagtcc	ctgtggagag	aacggcccat	tccaagggca	2100
ggaggatatt	gctctcggcc	tttgggaaac	ttttgagccg	agaggccgca	gacaggcatg	2160
tgggaggccc	agacacggca	ccctgccccg	tccaggacag	gcccaggacc	tgcccctctc	2220
tccacacctg	gggtacccct	tctcccccag	ccccaccact	actccaccca	ccttcctctc	2280
ctgagaccct	ccagccattc	cccttgaaaa	cacccccga	ccccaagcca	caataatgac	2340
agcgagagct	ccaattaact	aagcacctac	ctggcggcag	aataaccctt	cactgcctga	2400
tccccatctg	cagtgtggcc	caacagcccc	cagaactatg	cccacataga	ctggaggtag	2460
gcagttcacc	gtccctccct	gttaggaatg	agaccatccc	tgaggctatg	gcccaggccc	2520
acaggcgtcc	agtgtctgag	atctttggga	agggagacta	gggcaggtgg	agacagcgca	2580
gaacccccgt	gctgggtggg	aagcatgacc	acatggtggg	tgagcagccc	ccatgcactg	2640
acggtaaatt	cccctgtgga	ctcatttctg	ttggtttcta	ttacacctgg	ccaggcgtgg	2700
tacaatacag	gtcggtgctc	acaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	2760
aaa						2763
<210> 6 <211> 2054 <212> DNA	1					

<212> DNA <213> Homo Sapiens

<400> 6

60 ggaactggag caactggagc ttcgtggctc caaagtgcag acgctgtttc tcagcaaaaa ggagctgccg ggcgtgctgg agacagaggt cacctaccag ttcatcgacc agagcttcca 120 180 ggagttcctc gcggcactgt cctacctgct ggaggacggc ggggtgccca ggaccgcggc tggcggcgtt gggacactcc tgcgtgggga cgcccagccg cacagccact tggtgctcac 240

cacgcgcttc ctcttcggac tgctgagcgc ggagcggatg cgcgacatcg agcgccactt 300 360 cggctgcatg gtttcagagc gtgtgaagca ggaggccctg cggtgggtgc agggacaggg 420 acagggctgc cccggagtgg caccagaggt gaccgagggg gccaaagggc tcgaggacac 480 cgaagagcca gaggaggagg aggagggaga ggagcccaac tacccactgg agttgctgta 540 ctgcctgtac gagacgcagg aggacgcgtt tgtgcgccaa gccctgtgcc ggttcccgga 600 gctggcgctg cagcgagtgc gcttctgccg catggacgtg gctgttctga gctactgcgt 660 gaggtgctgc cctgctggac aggcactgcg gctgatcagc tgcagattgg ttgctgcgca 720 ggagaagaag aagaagagcc tggggaagcg gctccaggcc agcctgggtg gcggcagttc 780 tcaaggcacc acaaaacaac tgccagcctc ccttcttcat ccactctttc aggcaatgac tgacccactg tgccatctga gcagcctcac gctgtcccac tgcaaactcc ctgacgcggt 840 900 ctgccgagac ctttctgagg ccctgagggc agcccccgca ctgacggagc tgggcctcct ccacaacagg ctcagtgagg cgggactgcg tatgctgagt gagggcctag cctggccgca 960 1020 gtgcagggtg cagacggtca gggtacagct gcctgacccc cagcgagggc tccagtacct 1080 ggtgggtatg cttcggcaga gccccgccct gaccaccctg gatctcagcg gctgccaact gcccgccccc atggtgacct acctgtgtgc agtcctgcag caccagggat gcggcctgca 1140 1200 gaccctcagt ctggcctctg tggagctgag cgagcagtca ctacaggagc ttcaggctgt 1260 gaagagagca aagccggatc tggtcatcac acacccagcg ctggacggcc acccacaacc 1320 tcccaaggaa ctcatctcga ccttctgagg ctctggtggc cagagcaggg tggaagaccc 1380 tagtcaaagt ccctgtggag agaacggccc attccaaggg caggaggata ttgctctcgg 1440 cctttgggaa acttttgagc cgagaggccg cagacaggca tgtgggaggc ccagacacgg 1500 caccetgece egtecaggae aggeceagga cetgeceete tetecacace tggggtacee 1560 cttctccccc agccccacca ctactccacc caccttcctc tcctgagacc ctccagccat 1620 toccottgaa aacaccocco gaccocaago cacaataatg acagogagag otocaattaa ctaagcacct acctggggc agaataaccc ttcactgcct gatccccatc tgcagtgtgg 1680 cccaacagcc cccagaacta tgcccacata gactggaggt aggcagttca ccgtcctcc 1740 1800 ctgttaggaa tgagaccatc cctgaggcta tggcccaggc ccacaggcgt ccagtgtctg agatetttgg gaagggagae tagggeaggt ggagaeageg cagaaeeeee gtgetgggtg 1860 ggaagcatga ccacacggtg ggtgagcagc ccccatgcac tgatggtaaa ttcccctgtg 1920

```
gactcatttc tgttggtttc tattacacct ggccaggcgt ggtacaatac aggtcggtgc
2040
                                                               2054
aaaaaaaaa aaaa
<210> 7
<211> 314
<212> DNA
<213> homo sapiens
<220>
<221> misc feature
<222> (198)..(229)
<223> wherein "n" is equal to A, C, G, or T.
<220>
<221> misc_feature
     (289)..(289)
<222>
<223> n is a, c, g, or t
<400> 7
                                                                60
qccacttqqt qctcaccacq cqcttcctct tcggactgct gagcgcggag ggatgcgcga
categagege caettegget geatggttte agagegtgtg aageaggagg ceetgeggtg
                                                                120
ggtgcaggga cagggacagg gctgccccgg agtggcacca gaggtgaccg agggggccaa
                                                                180
                                                                240
agggctcgag gacaccgnnn nnnnnnnnn nnnnnnnnn nnnnnnnnn ccaactaccc
actggagttg ctgtactgcc tgtacgagac gcaggaggac gcgtttgtnc gccaaagccc
                                                                300
                                                                314
tgtgccggtt cccg
<210> 8
<211> 24
<212> PRT
<213> homo sapiens
<400> 8
Gly Ala Arg Val Leu Gly Gly Leu Leu Ser Lys Ala Leu Leu Pro Thr
Ala Leu Leu Leu Val Thr Thr Arg
<210>
      9
<211> 17
<212> PRT
<213> homo sapiens
```

1980

```
Leu Phe Ala Leu Cys Phe Val Pro Phe Val Cys Trp Ile Val Cys Thr
Val
<210> 10
<211> 17
<212> PRT
<213> homo sapiens
<400> 10
Ser Val Tyr Leu Leu Phe Ile Thr Ser Val Leu Ser Ser Ala Pro Val
Ala
<210> 11
<211>
       21
<212> DNA
<213> Homo sapiens
<400> 11
                                                                       21
catggtttca gagcgtgtga a
<210> 12
<211> 23
<212> DNA
<213> Homo sapiens
<400> 12
                                                                       23
tcgtacaggc agtacagcaa ctc
<210> 13
<211> 80
<212> DNA
<213> Homo sapiens
<400> 13
cttcacacgc tctgaaacca tgcagccgaa gtggcgctcg atgtcgcgca tccctccgcg
                                                                       80
ctcagcagtc cgaagaggaa
<210> 14
<211> 14
<212> PRT
```

<400> 9

```
<213> homo sapiens
<400> 14
Arg Phe Val Lys Glu Asn Glu Thr Leu Phe Ala Leu Cys Phe
<210> 15
<211> 17
<212> PRT
<213> homo sapiens
<400> 15
Phe Phe Arg Asp Glu Arg Ala Glu Arg Ala Tyr Arg Phe Val Lys
Glu
<210> 16
<211> 13
<212> PRT
<213> homo sapiens
<400> 16
Ala Leu Leu Val Thr Thr Arg Ala Ala Pro Gly
<210> 17
<211> 13
<212> PRT
<213> homo sapiens
<400> 17
Glu Val Arg Gly Phe Ser Asp Lys Asp Lys Lys Tyr
<210> 18
<211> 13
<212> PRT
<213> homo sapiens
<400> 18
Arg Asp Leu Ser Arg Thr Ser Lys Thr Thr Thr Ser Val
              5
                                 10
```

<210> 19

```
<211> 13
<212> PRT
<213> homo sapiens
<400> 19
Gln Thr Leu Phe Leu Ser Lys Lys Glu Leu Pro Gly Val
<210> 20
<211> 13
<212> PRT
<213> homo sapiens
<400> 20
Ser His Leu Val Leu Thr Thr Arg Phe Leu Phe Gly Leu
<210> 21
<211> 13
<212> PRT
<213> homo sapiens
<400> 21
Phe Gly Cys Met Val Ser Glu Arg Val Lys Gln Glu Ala
<210> 22
<211> 13
<212> PRT
<213> homo sapiens
<400> 22
Ala Leu Arg Leu Ile Ser Cys Arg Leu Val Ala Ala Gln
<210> 23
<211> 13
<212> PRT
<213> homo sapiens
<400> 23
Gly Ser Ser Gln Gly Thr Thr Lys Gln Leu Pro Ala Ser
                 5
<210> 24
<211> 13
<212> PRT
```

<213> homo sapiens

<400> 24

Gln Cys Arg Val Gln Thr Val Arg Val Gln Leu Pro Asp 1 5 10

<210> 25

<211> 514

<212> PRT

<213> homo sapiens

<400> 25

Gln Gln Met Glu Ser Gly Lys Ser Leu Ala Gln Thr Ser Lys Thr Ser 20 25 30

Thr Ala Val Tyr Val Phe Phe Leu Ser Ser Leu Leu Gln Pro Arg Gly 35 40 45

Gly Ser Gln Glu His Gly Leu Cys Ala His Leu Trp Gly Leu Cys Ser 50 55 60

Leu Ala Ala Asp Gly Ile Trp Asn Gln Lys Ile Leu Phe Glu Glu Ser 65 70 75 80

Asp Leu Arg Asn His Gly Leu Gln Lys Ala Asp Val Ser Ala Phe Leu 85 90 95

Arg Met Asn Leu Phe Gln Lys Glu Val Asp Cys Glu Lys Phe Tyr Ser 100 105 110

Phe Ile His Met Thr Phe Gln Glu Phe Phe Ala Ala Met Tyr Tyr Leu 115 120 125

Leu Glu Glu Glu Lys Glu Gly Arg Thr Asn Val Pro Gly Ser Arg Leu 130 135 140

Lys Leu Pro Ser Arg Asp Val Thr Val Leu Leu Glu Asn Tyr Gly Lys 145 150 155

Phe Glu Lys Gly Tyr Leu Ile Phe Val Val Arg Phe Leu Phe Gly Leu 165 170 175 Val Asn Gln Glu Arg Thr Ser Tyr Leu Glu Lys Lys Leu Ser Cys Met 180 185 Ile Ser Gln Gln Ile Arg Leu Glu Leu Leu Lys Trp Ile Glu Val Lys 200 Ala Lys Ala Lys Leu His Asp Gln Pro Ser Gln Leu Glu Leu Phe 220 Tyr Cys Leu Tyr Glu Met Gln Glu Glu Asp Phe Val Gln Arg Ala Met 235 230 Asp Tyr Phe Pro Lys Ile Glu Ile Asn Leu Ser Thr Arg Met Asp His 250 Met Val Ser Ser Phe Cys Ile Glu Asn Cys His Arg Val Glu Ser Leu Ser Leu Gly Phe Leu His Asn Met Pro Lys Glu Glu Glu Glu Glu Glu 280 Lys Glu Gly Arg His Leu Asp Met Val Gln Cys Val Leu Pro Ser Ser Ser His Ala Ala Cys Ser His Gly Leu Gly Arg Cys Gly Leu Ser His Glu Cys Cys Phe Asp Ile Ser Leu Val Leu Ser Ser Asn Gln Lys Leu 330 Val Glu Leu Asp Leu Ser Asp Asn Ala Leu Gly Asp Phe Gly Ile Arg 345 Leu Leu Cys Val Gly Leu Lys His Leu Leu Cys Asn Leu Lys Lys Leu 360 Trp Leu Val Asn Ser Ala Leu Arg Gln Ser Val Val Gln Leu Cys Pro 370 375 380 Arg Tyr Ser Ala Leu Ile Arg Ile Ser Arg Thr Phe Thr Ala Arg Gln 385 390 395

His Ser Arg Arg Gln Gly Ile Lys Leu Leu Cys Glu Gly Leu Leu His 405 410 415

Pro Asp Cys Lys Leu Gl
n Val Leu Glu Leu Asp Asn Cys Asn Leu Thr $420 \hspace{1.5cm} 425 \hspace{1.5cm} 430$

Ser His Cys Cys Trp Asp Leu Ser Thr Leu Leu Thr Ser Ser Gln Ser 435 440 445

Leu Arg Lys Leu Ser Leu Gly Asn Asn Asp Leu Gly Asp Leu Gly Val 450 455 460

Met Met Phe Cys Glu Val Leu Lys Gln Gln Ser Cys Leu Leu Gln Asn 465 470 475 480

Leu Gly Leu Ser Glu Met Tyr Phe Asn Tyr Glu Thr Lys Ser Ala Leu 485 490 495

Glu Thr Leu Gln Glu Glu Lys Pro Glu Leu Thr Val Val Phe Glu Pro 500 505 510

Ser Trp

<210> 26

<211> 1429

<212> PRT

<213> homo sapiens

<400> 26

Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu 1 5 10 15

Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala As
n Lys Ala 20 25 30

His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr 35 40 45

Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln 50 55 60

Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg

Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe 85 90 95

Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr 100 105 110

Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys 115 120 125

Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser 130 135 140

Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala 165 170 175

Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro 180 185 190

Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu 195 200 205

Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg 210 $\,$ 220 $\,$

Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr 225 230 235 240

Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu 245 250 255

Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu 260 265 270

Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Gln Arg Pro His 275 280 285

Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val 290 295 300

Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro 310 315 Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly 345 Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser 355 360 Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile 375 Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser 390 395 Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly 405 410 Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln 425 420 Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln 455 Aşn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly 470 475 Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu 500 505 Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr 525 515 520

Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser Lys Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val Pro Ser Leu Gln Leu Leu Gln Pro His Ser Leu Glu Ser Leu His Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu

- Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln 755 760 765
- Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val 770 780
- Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu 785 790 795 800
- Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser 805 810 815
- Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu 820 825 830
- Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly 835 840 845
- Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn 850 855 860
- Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala 865 870 875 880
- Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu 885 890 895
- Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln 900 905 910
- Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp 915 920 925
- Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu 930 935 940
- Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln 945 . 950 955 960
- Thr Thr Leu Ser Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln 965 970 975
- Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met

980 985 990

- Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser 995 1000 1005
- Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His 1010 1015 1020
- Val Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe 1025 1030 1035
- Pro Ile Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro 1040 1045 1050
- Val Glu Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu 1055 1060 1065
- His Thr Lys Pro Leu Gly Thr Asp Asp Asp Phe Trp Gly Pro Thr 1070 1075 1080
- Gly Pro Val Ala Thr Glu Val Val Asp Lys Glu Lys Asn Leu Tyr 1085 1090 1095
- Arg Val His Phe Pro Val Ala Gly Ser Tyr Arg Trp Pro Asn Thr 1100 1105 1110
- Gly Leu Cys Phe Val Met Arg Glu Ala Val Thr Val Glu Ile Glu 1115 1120 1125
- Phe Cys Val Trp Asp Gln Phe Leu Gly Glu Ile Asn Pro Gln His 1130 1135 1140
- Ser Trp Met Val Ala Gly Pro Leu Leu Asp Ile Lys Ala Glu Pro 1145 1150 1155
- Gly Ala Val Glu Ala Val His Leu Pro His Phe Val Ala Leu Gln 1160 . 1165 . 1170
- Gly Gly His Val Asp Thr Ser Leu Phe Gln Met Ala His Phe Lys 1175 1180 1185
- Glu Glu Gly Met Leu Leu Glu Lys Pro Ala Arg Val Glu Leu His 1190 1195 1200

His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro Leu Gly Val Leu Leu Lys Met Ile His Asn Ala Leu Arg Phe Ile Pro Val Thr Ser Val Val Leu Leu Tyr His Arg Val His Pro Glu Glu Val Thr Phe His Leu Tyr Leu Ile Pro Ser Asp Cys Ser Ile Arg Lys Glu Leu Glu Leu Cys Tyr Arg Ser Pro Gly Glu Asp Gln Leu Phe Ser Glu Phe Tyr Val Gly His Leu Gly Ser Gly Ile Arg Leu Gln Val Lys Asp Lys Lys Asp Glu Thr Leu Val Trp Glu Ala Leu Val Lys Pro Gly Asp Leu Met Pro Ala Thr Thr Leu Ile Pro Pro Ala Arg Ile Ala Val Pro Ser Pro Leu Asp Ala Pro Gln Leu Leu His Phe Val Asp Gln Tyr Arg Glu Gln Leu Ile Ala Arg Val Thr Ser Val Glu Val Val Leu Asp Lys Leu His Gly Gln Val Leu Ser Gln Glu Gln Tyr Glu Arg Val Leu Ala Glu Asn Thr Arg Pro Ser Gln Met Arg Lys Leu Phe Ser Leu Ser Gln Ser Trp Asp Arg Lys Cys Lys Asp Gly Leu Tyr Gln Ala Leu Lys Glu Thr His Pro His Leu Ile Met

Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu Leu Pro Leu Ser 1415 1420 1425

Ser

<210> 27 <211> 8 <212> PRT <213> bact	eriophage 1	r7													
<400> 27															
Asp Tyr Lys	Asp Tyr Lys Asp Asp Asp Lys 1 5														
<210> 28 <211> 733 <212> DNA <213> homo	sapiens														
<400> 28 gggatccgga	gcccaaatct	tctgacaaaa	ctcacacatg	cccaccgtgc	ccagcacctg	60									
aattcgaggg	tgcaccgtca	gtcttcctct	tccccccaaa	acccaaggac	accctcatga	120									
tctcccggac	tcctgaggtc	acatgcgtgg	tggtggacgt	aagccacgaa	gaccctgagg	180									
tcaagttcaa	ctggtacgtg	gacggcgtgg	aggtgcataa	tgccaagaca	aagccgcggg	240									
aggagcagta	caacagcacg	taccgtgtgg	tcagcgtcct	caccgtcctg	caccaggact	300									
ggctgaatgg	caaggagtac	aagtgcaagg	tctccaacaa	agccctccca	acccccatcg	360									
agaaaaccat	ctccaaagcc	aaagggcagc	cccgagaacc	acaggtgtac	accctgcccc	420									
catcccggga	tgagctgacc	aagaaccagg	tcagcctgac	ctgcctggtc	aaaggcttct	480									
atccaagcga	catcgccgtg	gagtgggaga	gcaatgggca	gccggagaac	aactacaaga	540									
ccacgcctcc	cgtgctggac	tccgacggct	ccttcttcct	ctacagcaag	ctcaccgtgg	600									
acaagagcag	gtggcagcag	gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	660									
acaaccacta	cacgcagaag	agcctctccc	tgtctccggg	taaatgagtg	cgacggccgc	720									
gactctagag	gat					733									

<210> 29 <211> 39 <212> DNA <213> Homo sapiens

<400 gca		29 cgg (ccgc	gacg	gg c	cccg	gttg	c ag	ggcg	acc							39
<210 <211 <212 <213	1> 2>	30 37 DNA Homo	sap	iens													
<400 gca		30 tcg a	acag	aagg [.]	tc g	agat	gagt [.]	t cc	ttgg	g							37
<210 <211 <212 <213	l> 2>	31 39 DNA Homo	sap:	iens													
<400 gca		31 cgg (ccgc	atgc	tg g	ccca	gccg	c ago	cggc	tgc							39
<210 <211 <212 <213	L> 2>	32 37 DNA Homo	sap:	iens													
<400 gcag		32 tcg a	acato	ccag	gg to	ggtc	agggo	c gg	ggct	С							37
<210> 33 <211> 1032 <212> PRT <213> Homo sapiens																	
<400)> .	33															
Met 1	Ala	Ser	Thr	Arg 5	Cys	Lys	Arg	Tyr	Leu 10	Glu	Asp	Leu	Glu	Asp 15	Val		
Asp	Leu	Lys	Lys 20	Phe	Lys	Met	His	Leu 25	Glu	Asp	Tyr	Pro	Pro 30	Gln	Lys		
Gly	Cys	Ile 35	Pro	Leu	Pro	Arg	Gly 40	Gln	Thr	Glu	Lys	Ala 45	Asp	His	Val		
Asp	Leu 50	Ala	Thr	Leu	Met	Ile 55	Asp	Phe	Asn	Gly	Glu 60	Glu	Lys	Ala	Trp		
Ala 65	Met	Ala	Val	Trp	Ile 70	Phe	Ala	Ala	Ile	Asn 75	Arg	Arg	Asp	Leu	Tyr 80		

- Glu Lys Ala Lys Arg Asp Glu Pro Lys Trp Gly Ser Asp Asn Ala Arg 85 90 95
- Val Ser Asn Pro Thr Val Ile Cys Gln Glu Asp Ser Ile Glu Glu Glu 100 105 110
- Trp Met Gly Leu Leu Glu Tyr Leu Ser Arg Ile Ser Ile Cys Lys Met 115 120 125
- Lys Lys Asp Tyr Arg Lys Lys Tyr Arg Lys Tyr Val Arg Ser Arg Phe 130 . 135 140
- Gln Cys Ile Glu Asp Arg Asn Ala Arg Leu Gly Glu Ser Val Ser Leu 145 150 155 160
- Asn Lys Arg Tyr Thr Arg Leu Arg Leu Ile Lys Glu His Arg Ser Gln 165 170 175
- Gln Glu Arg Glu Gln Glu Leu Leu Ala Ile Gly Lys Thr Lys Thr Cys 180 185 190
- Glu Ser Pro Val Ser Pro Ile Lys Met Glu Leu Leu Phe Asp Pro Asp 195 200 205
- Asp Glu His Ser Glu Pro Val His Thr Val Val Phe Gln Gly Ala Ala 210 215 220
- Gly Ile Gly Lys Thr Ile Leu Ala Arg Lys Met Met Leu Asp Trp Ala 225 230 235 . 240
- Ser Gly Thr Leu Tyr Gln Asp Arg Phe Asp Tyr Leu Phe Tyr Ile His 245 250 255
- Cys Arg Glu Val Ser Leu Val Thr Gln Arg Ser Leu Gly Asp Leu Ile 260 265 270
- Met Ser Cys Cys Pro Asp Pro Asn Pro Pro Ile His Lys Ile Val Arg 275 280 285
- Lys Pro Ser Arg Ile Leu Phe Leu Met Asp Gly Phe Asp Glu Leu Gln 290 295 300

Gly Ala Phe Asp Glu His Ile Gly Pro Leu Cys Thr Asp Trp Gln Lys Ala Glu Arg Gly Asp Ile Leu Leu Ser Ser Leu Ile Arg Lys Lys Leu Leu Pro Glu Ala Ser Leu Leu Ile Thr Thr Arg Pro Val Ala Leu Glu Lys Leu Gln His Leu Leu Asp His Pro Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala Lys Arg Lys Glu Tyr Phe Phe Lys Tyr Phe Ser Asp Glu Ala Gln Ala Arg Ala Ala Phe Ser Leu Ile Gln Glu Asn Glu Val Leu Phe Thr Met Cys Phe Ile Pro Leu Val Cys Trp Ile Val Cys Thr Gly Leu Lys Gln Gln Met Glu Ser Gly Lys Ser Leu Ala Gln Thr Ser Lys Thr Thr Thr Ala Val Tyr Val Phe Phe Leu Ser Ser Leu Leu Gln Pro Arg Gly Gly Ser Gln Glu His Gly Leu Cys Ala His Leu Trp Gly Leu Cys Ser Leu Ala Ala Asp Gly Ile Trp Asn Gln Lys Ile Leu Phe Glu Glu Ser Asp Leu Arg Asn His Gly Leu Gln Lys Ala Asp Val Ser Ala Phe Leu Arg Met Asn Leu Phe Gln Lys Glu Val Asp Cys Glu Lys Phe Tyr Ser Phe Ile His Met Thr Phe Gln Glu Phe Phe Ala Ala Met

Tyr Tyr Leu Leu Glu Glu Glu Lys Glu Gly Arg Thr Asn Val Pro Gly Ser Arg Leu Lys Leu Pro Ser Arg Asp Val Thr Val Leu Leu Glu Asn Týr Gly Lys Phe Glu Lys Gly Tyr Leu Ile Phe Val Val Arg Phe Leu Phe Gly Leu Val Asn Gln Glu Arg Thr Ser Tyr Leu Glu Lys Lys Leu Ser Cys Lys Ile Ser Gln Gln Ile Arg Leu Glu Leu Leu Lys Trp Ile Glu Val Lys Ala Lys Ala Lys Lys Leu Gln Ile Gln Pro Ser Gln Leu Glu Leu Phe Tyr Cys Leu Tyr Glu Met Gln Glu Glu Asp Phe Val Gln Arg Ala Met Asp Tyr Phe Pro Lys Ile Glu Ile Asn Leu Ser Thr Arg Met Asp His Met Val Ser Ser Phe Cys Ile Glu Asn Cys His Arg Val Glu Ser Leu Ser Leu Gly Phe Leu His Asn Met Pro Lys Glu Glu Glu Glu Glu Glu Lys Glu Gly Arg His Leu Asp Met Val Gln Cys Val Leu Pro Ser Ser His Ala Ala Cys Ser His Gly Leu Val Asn Ser His Leu Thr Ser Ser Phe Cys Arg Gly Leu Phe Ser Val Leu Ser Thr Ser Gln Ser Leu Thr Glu Leu Asp Leu Ser Asp Asn Ser Leu Gly Asp Pro

Gly Met Arg Val Leu Cys Glu Thr Leu Gln His Pro Gly Cys Asn Ile

755 760 765

Arg Arg Leu Trp Leu Gly Arg Cys Gly Leu Ser His Glu Cys Cys Phe 770 780

Asp Ile Ser Leu Val Leu Ser Ser Asn Gln Lys Leu Val Glu Leu Asp 785 790 795 800

Leu Ser Asp Asn Ala Leu Gly Asp Phe Gly Ile Arg Leu Leu Cys Val805 810 815

Gly Leu Lys His Leu Leu Cys Asn Leu Lys Lys Leu Trp Leu Val Ser 820 825 830

Cys Cys Leu Thr Ser Ala Cys Cys Gln Asp Leu Ala Ser Val Leu Ser 835 840 845

Thr Ser His Ser Leu Thr Arg Leu Tyr Val Gly Glu Asn Ala Leu Gly 850 855 860

Asp Ser Gly Val Ala Ile Leu Cys Glu Lys Ala Lys Asn Pro Gln Cys 865 870 875 888

Asn Leu Gln Lys Leu Gly Leu Val Asn Ser Gly Leu Thr Ser Val Cys 885 890 895

Cys Ser Ala Leu Ser Ser Val Leu Ser Thr Asn Gln Asn Leu Thr His
900 905 910

Leu Tyr Leu Arg Gly Asn Thr Leu Gly Asp Lys Gly Ile Lys Leu Leu 915 920 925

Cys Glu Gly Leu Leu His Pro Asp Cys Lys Leu Gl
n Val Leu Glu Leu 930 935 940

Asp Asn Cys Asn Leu Thr Ser His Cys Cys Trp Asp Leu Ser Thr Leu 945 950 955 960

Leu Thr Ser Ser Gln Ser Leu Arg Lys Leu Ser Leu Gly Asn Asn Asp 965 970 975

Leu Gly Asp Leu Gly Val Met Met Phe Cys Glu Val Leu Lys Gln Gln 980 985 990

1000 Glu Thr Lys Ser Ala Leu Glu Thr Leu Gln Glu Glu Lys Pro Glu 1015 1010 Leu Thr Val Val Phe Glu Pro Ser Trp <210> 34 <211> 25 <212> DNA <213> artificial <220> <223> Synthesized oligonucleotide. <400> 34 25 cctctcatcc cggaagaacu uguag <210> 35 <211> 25 <212> DNA <213> artificial <220> <223> Synthesized oligonucleotide. <400> 35 25 ggcctcctgc uucacacgcu cugaa <210> 36 <211> 25 <212> DNA <213> artificial <220> <223> Synthesized oligonucleotide. <400> 36 25 aactcctgga agcucugguc gauga <210> 37 <211> 25 <212> DNA <213> artificial <220>

Ser Cys Leu Leu Gln Asn Leu Gly Leu Ser Glu Met Tyr Phe Asn Tyr

<223> Synthesized oligonucleotide.

```
<400> 37
                                                                     25
gtctgcactu uggagccacg aagct
<210> 38
<211> 25
<212> DNA
<213> artificial
<220>
<223> Synthesized oligonucleotide.
<400> 38
                                                                     25
ttctccttca cgaagcggua ggcgc
<210>
      39
<211>
      24
<212>
      DNA
<213> Homo sapiens
<400> 39
                                                                     24
gaggatgagg agagctatga caca
<210> 40
<211>
      22
<212> DNA
<213> Homo sapiens
<400> 40
ccctttgcac tcataacgtc ag
                                                                     22
<210>
      41
<211> 29
<212>
      DNA
<213> Homo sapiens
<400> 41
                                                                     29
aaacacacag tcatcatagg gcagctcgt
<210>
      42
<211>
      20
<212> PRT
<213> Artificial Sequence
<220>
<223> Concensus Sequence.
<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> wherein "X" equals any naturally occuring amino acids
```

```
<220>
<221> MISC FEATURE
<222> (12)..(12)
<223> wherein "X" equals either "leucine" or other naturally occuring
       aliphatic amino acid residue.
<220>
<221> MISC FEATURE
<222>
      (13)..(15)
<223> wherein "X" equals any naturally occuring amino acids
<220>
<221> MISC_FEATURE
<222>
      (16)..(16)
<223> wherein "X" equals either "leucine" or other naturally occuring
       aliphatic amino acid residue.
<220>
<221>
      MISC_FEATURE
<222>
      (17)..(20)
      wherein "X" equals any naturally occuring amino acids
<223>
<400> 42
Xaa Leu Xaa Xaa Leu Xaa Leu Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa
                                    10
                5
Xaa Xaa Leu Xaa
<210>
      43
<211>
      24
<212>
      PRT
<213> Artificial Sequence
<220>
<223> Concensus Sequence.
<220>
<221>
      MISC_FEATURE
<222>
      (1)..(20)
<223>
      wherein "X" equals any naturally occuring amino acid.
<220>
<221>
      MISC FEATURE
<222>
      (21)..(21)
<223> wherein "X" equals any naturally occuring non-polar amino acid
       residue.
<220>
<221> MISC FEATURE
<222> (22)..(24)
<223> wherein "X" equals any naturally occuring amino acid.
```

```
Leu Xaa Xaa Leu Xaa Leu Xaa Leu Xaa Xaa Asn Xaa Leu Xaa Xaa
                5
Leu Pro Xaa Xaa Xaa Phe Xaa Xaa
           20
<210> 44
<211> 8
<212> PRT
<213> Artificial Sequence
<220>
<223> Concensus Sequence.
<220>
      MISC_FEATURE
<221>
<222>
      (1)..(1)
<223>
      wherein "X" equals either "arginine" or "lysine".
<220>
<221> MISC_FEATURE
<222>
      (2)..(3)
<223> wherein "X" equals any naturally occuring amino acid residue.
<220>
<221>
      MISC_FEATURE
<222>
      (4)..(4)
<223>
      wherein "X" equals either "aspartic acid" or "glutamic acid".
<220>
<221> MISC_FEATURE
<222>
      (5)..(7)
<223> wherein "X" equals any naturally occuring amino acid residue.
<220>
<221> misc_feature
<222>
      (8)..(8)
<223>
      Xaa can be any naturally occurring amino acid
<400> 44
Xaa Xaa Xaa Xaa Xaa Xaa Xaa
<210> 45
      8
<211>
<212> PRT
<213> Artificial Sequence
```

<400> 43

<220>

```
<223> Concensus Sequence.
<220>
<221> MISC_FEATURE
<222>
      (1)..(1)
<223> wherein "X" equals either "arginine" or "lysine".
<220>
<221> MISC_FEATURE
<222>
      (2)..(4)
<223> wherein "X" equals any naturally occuring amino acid.
<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> wherein "X" equals either "aspardic acid" or "glutamic acid".
<220>
<221> MISC_FEATURE
<222>
      (6)..(7)
<223> wherein "X" equals any naturally occuring amino acid residue..
<220>
<221> misc_feature
<222>
      (8)..(8)
<223> Xaa can be any naturally occurring amino acid
<400> 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa
```